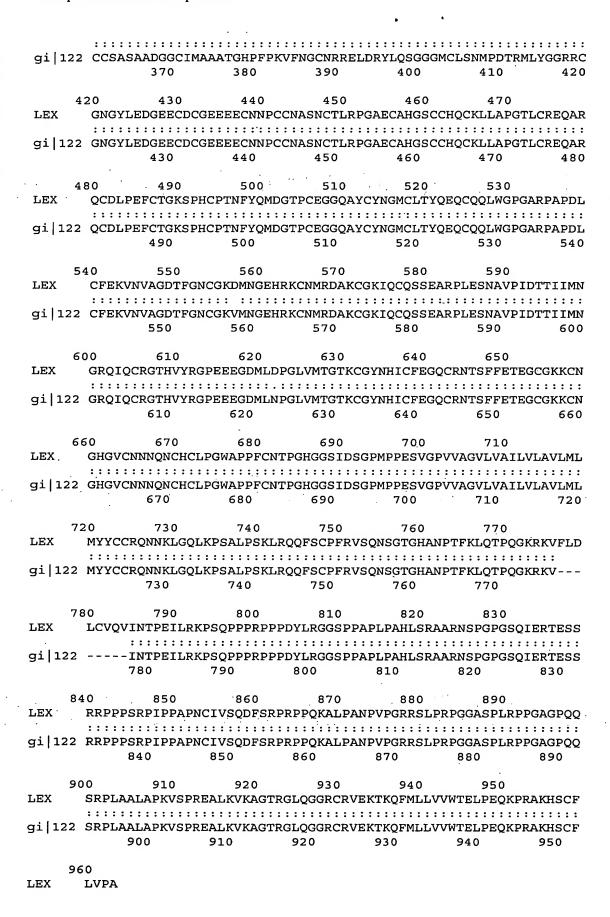
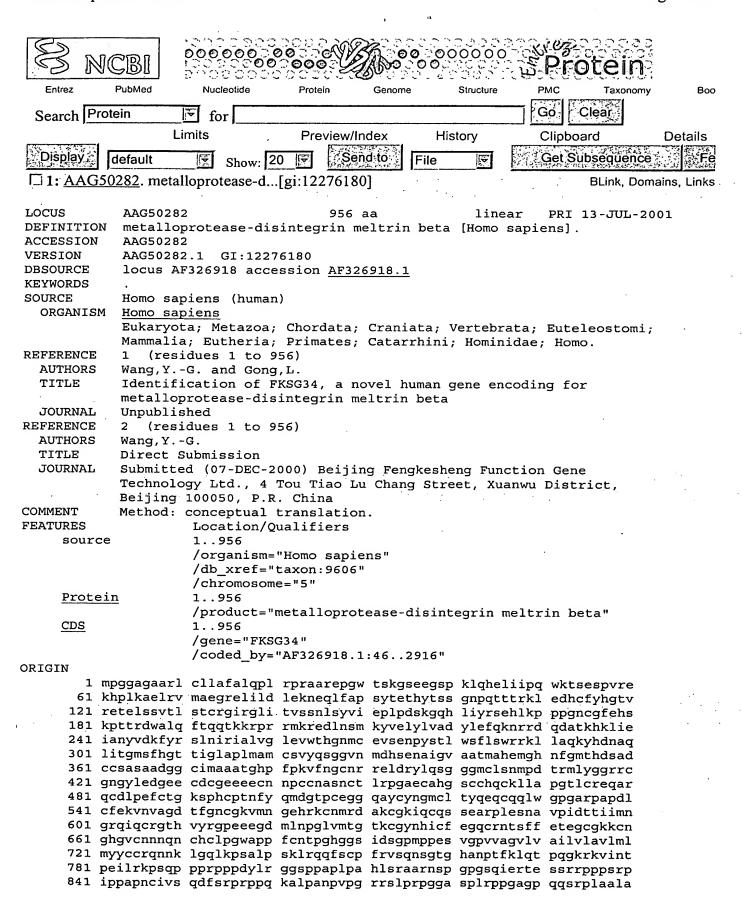
```
B 500%
     FASTA searches a protein or DNA sequence data bank
     veration 3.3t05 March 30, 2000
    Please cite:
/tmp/fastaGAAosaW1G: 963 aa
     >LEX 263 SEQ ID NO:2
       /tmp/fastaHAApsaW1G library
    searching /tmp/fastaHAApsaWlG library
                       1 sequences
       956 residues in
    FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
    join: 39, opt: 27, gap-pen: -12/ -2, width: 16
    Scan time: 0.033
    The best scores are:
                                                     opt
    gi|12276180|gb|AAG50282.1|AF326918_1 metalloprote
                                              (956) 6778
    >>gi|12276180|gb|AAG50282.1|AF326918 1 metalloprotease-d (956 aa)
    initn: 5376 init1: 5315 opt: 6778
    Smith-Waterman score: 6778; 98.755% identity in 964 aa overlap (1-963:1-956)
                                                  50
                        20
                                 30
                                          40
    LEX
         MPGGAGAARLCLLAFALQPLRPRAAREPGWT-RGSEEGSPKLQHELIIPQWKTSESPVRE
         gi|122 MPGGAGAARLCLLAFALQPLRPRAAREPGWTSKGSEEGSPKLQHELIIPQWKTSESPVRE
                        20
                                 30
                                         40
                                                          60
        60
                         80
                                 90
                                         100
   LEX
         KHPLKAELRVMAEGRELILDLEKNEQLFAPSYTETHYTSSGNPQTTTRKLEDHCFYHGTV
         gi | 122 KHPLKAELRVMAEGRELILDLEKNEQLFAPSYTETHYTSSGNPQTTTRKLEDHCFYHGTV
                70
                        80 .
                                90
                                        100
                                                 110
                                                         120
                        140
                                150
                                         160
        120
                130
         RETELSSVTLSTCRGIRGLITVSSNLSYVIEPLPDSKGQHLIYRSEHLKPPPGNCGFEHS
   LEX
         qi|122 RETELSSVTLSTCRGIRGLITVSSNLSYVIEPLPDSKGQHLIYRSEHLKPPPGNCGFEHS
                                        160
                                                170
                                                         180
               130
                       140
                                150
                                210
                                         220
                                                 230
        180
                190
                        200
   LEX
         KPTTRDWALQFTQQTKKRPRRMKREDLNSMKYVELYLVADYLEFQKNRRDQDATKHKLIE
         gi|122 KPTTRDWALQFTQQTKKRPRRMKREDLNSMKYVELYLVADYLEFQKNRRDQDATKHKLIE
               190
                       200
                                210
                                        220
                                                230
                                                         240
                                270
                                         280
                250
                        260
   LEX
         IANYVDKFYRSLNIRIALVGLEVWTHGNMCEVSENPYSTLWSFLSWRRKLLAQKYHDNAQ
         gi|122 IANYVDKFYRSLNIRIALVGLEVWTHGNMCEVSENPYSTLWSFLSWRRKLLAQKYHDNAQ
               250
                       260
                                270
                                        280
                                                290
                                         340
                310
                        320
                                330
   LEX
         LITGMSFHGTTIGLAPLMAMCSVYQSGGVNMDHSENAIGVAATMAHEMGHNFGMTHDSAD
         gi|122 LITGMSFHGTTIGLAPLMAMCSVYQSGGVNMDHSENAIGVAATMAHEMGHNFGMTHDSAD
               310
                       320
                               330
                                        340
                                                350
                                                         360
                370
                        380
                                390
                                         400
         CCSASAADGGCIMAAATGHPFPKVFNGCNRRELDRYLQSGGGMCLSNMPDTRMLYGGRRC
   LEX
```



:::: gi|122 LVPA

963 residues in 1 query sequences 956 residues in 1 library sequences Scomplib [version 3.3t05 March 30, 2000] start: Thu Mar 11 14:41:49 2004 done: Thu Mar 11 14:41:50 2004 Scan time: 0.033 Display time: 1.317

Function used was FASTA



//

901 pkvsprealk vkagtrglqg grcrvektkq fmllvvwtel peqkprakhs cflvpa

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Feb 24 2004 16:01:25